

【Sequence listing】

<110> Scigen Harvest Co., Ltd.

<120> Genes for S-adenosyl L-methionine:jasmonic acid carboxyl methyl transferase and a method for the development of pathogen- and stress-resistant plants using the genes

<130> OPF0154

<150> KR

<151> 2000-06-13

<160> 5

<170> KopatentIn 1.71

<210> 1

<211> 1170

<212> DNA

<213> Arabidopsis thaliana

<400> 1

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aagaagttaa tgatgagcaa ttcagagatt tcgagcattg gaatcgccga cttaggtctgc	180
tcctccggtc cgaacagtct cttgtccatc tccaacatag ttgacacgat ccacaacttg	240
tgtctgacc tcgaccgtcc agtcctgag ctgagagtct ctctcaacga cctccctagc	300
aatgacttca actacatatg tgcttcttg ccagagtttt acgaccgggt taataataac	360
aaggaggggt taggggtcgg tcgtggagga ggagaatcgt gttttgtgtc ggccgtccca	420
ggttcgttct acggacgttt gtttcctcgc cggagccttc actttgtgca ttcttcttct	480
agtttacatt ggttgtctca ggttccatgt cgtgaggcgg agaaggaaga caggacaata	540
acagctgatt tagaaaacat ggggaaaata tacatatcaa agacaagtcc taagagtgc	600
cataaagctt atgctcttca attccaaact gatttcttgg ttttttgag gtcacgatct	660
gaggagtgg tcccgggagg ccgaatggtt ttatcgttcc ttggtagaag atcactggat	720
cccacaaccg aagagagttg ctatcaatgg gaactcctag ctcaagctct tatgtccatg	780

gccaaagagg gtatcatcga ggaagagaag atcgatgctt tcaacgctcc ttactatgct 840
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cttgagataa gtccgattga ttgggaaggt gggagtatca gtgaggagag ttatgacctt 960
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<210> 2
<211> 1476
<212> DNA
<213> Arabidopsis thaliana
<220>
<221> CDS
<222> (15)..(1181)
<223> open reading frame for JMT

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gga aac ggg gaa aca agt tat gcc aag aac tcc acc gct cag agc aac 95
Gly Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn
15 20 25
ata ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta 143
Ile Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu
30 35 40
atg atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc 191
Met Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly
45 50 55
tgc tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac 239
Cys Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp
60 65 70 75
acg atc cac aac ttg tgt cct gac ctc gac cgt cca gtc cct gag ctc 287
Thr Ile His Asn Leu Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu
80 85 90

aga gtc tct ctc aac gac ctc cct agc aat gac ttc aac tac ata tgt	335
Arg Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys	
95 100 105	
gct tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt	383
Ala Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly	
110 115 120	
tta ggg ttc ggt cgt gga gga gga gaa tcg tgt ttt gtg tcg gcc gtc	431
Leu Gly Phe Gly Arg Gly Gly Glu Ser Cys Phe Val Ser Ala Val	
125 130 135	
cca ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt	479
Pro Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe	
140 145 150 155	
gtg cat tct tct tct agt tta cat tgg ttg tct cag gtt cca tgt cgt	527
Val His Ser Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg	
160 165 170	
gag gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg	575
Glu Ala Glu Lys Glu Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met	
175 180 185	
ggg aaa ata tac ata tca aag aca agt cct aag agt gca cat aaa gct	623
Gly Lys Ile Tyr Ile Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala	
190 195 200	
tat gct ctt caa ttc caa act gat ttc ttg gtt ttt ttg agg tca cga	671
Tyr Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg	
205 210 215	
tct gag gag ttg gtc ccg gga ggc cga atg gtt tta tcg ttc ctt ggt	719
Ser Glu Glu Leu Val Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly	
220 225 230 235	
aga aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa	767
Arg Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu	
240 245 250	
ctc cta gct caa gct ctt atg tcc atg gcc aaa gag ggt atc atc gag	815
Leu Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu	
255 260 265	
gaa gag aag atc gat gct ttc aac gct cct tac tat gct gcg agc tcc	863
Glu Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser	
270 275 280	
gaa gag ttg aaa atg gtg ata gag aaa gaa ggg tca ttt tcg atc gat	911

Glu Glu Leu Lys Met Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp
 285 290 295
 agg ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag 959
 Arg Leu Glu Ile Ser Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu
 300 305 310 315
 gag agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt 1007
 Glu Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser
 320 325 330
 ggc cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta 1055
 Gly Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu
 335 340 345
 gaa cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat 1103
 Glu Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr
 350 355 360
 gca aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct 1151
 Ala Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala
 365 370 375
 att gtt att ctt tcg ctc gtt aga acc ggt tgatcgtgt tataacatat 1200
 Ile Val Ile Leu Ser Leu Val Arg Thr Gly
 380 385
 gccaatatac atgtctttgg gcctacaatg acatgatttg gtagttttct aatcaagcat 1260
 atgtaatata atttgcttcg agaataaaat aataaaataa agtgtgatgt tacggtagac 1320
 cctttttttt tttttctcat ttacggtaga cctatagtat taaaacaaat agaatcagct 1380
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 <211> 389
 <212> PRT
 <213> Arabidopsis thaliana

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 Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile Ile Ser Leu Gly
 20 25 30

Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met Met Ser Asn Ser
35 40 45

Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
50 55 60

Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
65 70 75 80

Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
85 90 95

Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
100 105 110

Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
115 120 125

Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
130 135 140

Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val His Ser Ser Ser
145 150 155 160

Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
165 170 175

Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
180 185 190

Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
195 200 205

Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
210 215 220

Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
225 230 235 240

Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
245 250 255

Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
260 265 270

Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
275 280 285

Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
290 295 300

Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
305 310 315 320

Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
325 330 335

Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
340 345 350

Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
355 360 365

Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile Val Ile Leu Ser
370 375 380

Leu Val Arg Thr Gly
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<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer for PCR of JMT gene

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<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer for PCR of JMT gene

<400> 5
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